

0280

#2

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/825,580

DATE: 04/19/2001
TIME: 12:17:56

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\04192001\I825580.raw

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3 <110> APPLICANT: Eppihimer, Michael J.
4     Schaub, Robert G.
5     Harris, Alan
7 <120> TITLE OF INVENTION: Inhibition of Thrombosis by Treatment with
8     P-Selectin Antagonists
10 <130> FILE REFERENCE: GFN-5398
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/825,580
C--> 13 <141> CURRENT FILING DATE: 2001-04-02
15 <150> PRIOR APPLICATION NUMBER: 60/193,787
16 <151> PRIOR FILING DATE: 2000-03-31
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1649
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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32 gggacacctg ggcagatgaa gccgagaaag ccttgggtcc cctgcttgcc cgggaccgga 180
34 gacaggccac cgaatatgag tacctagatt atgatttcc tccagaaacg gagcctccag 240
36 aaatgctgag gaacagcact gacaccactc ctctgactgg gcctggaacc cctgagtcta 300
38 ccactgtgga gctgctgca aggcgttcta ctggcctgga tgcaggaggg gcagtacaga 360
40 agctgaccac tgaactggcc aacatgggga acctgtccac ggattcagca gctatggaga 420
42 tacagaccac tcaaccagca gccacggagg cacagaccac tccactggca gccacagagg 480
44 cacagacaac tcgactgacg gccacggagg cacagaccac tccactggca gccacagagg 540
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48 cacagaccac tgcaccagca gccatggagg cacagaccac tgcaccagca gccatggaag 660
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52 cacagaccac tgcaccagaa gccacggagg cacagaccac tcaaccaca gccacggagg 780
54 cacagaccac tccactggca gccatggagg cctgttccac agaaccagc gccacagagg 840
56 cctgttccat ggaacctact accaaaagag gtctgttccat acccttttct gtgtcctctg 900
58 ttactcaaa gggcattccc atggcagcca gcaatttctc cgtcaactac ccagtggggg 960
60 cccagacca catctctgtg aagcagtgcc tgctggccat cctaactctg gcgctggtg 1020
62 ccaactatct cttcgtgtgc actgtggtgc tggcgggtcc cctctcccgc aagggccaca 1080
64 tgtaccccgt gcgtaattac tccccaccg agatggtctg catctcatcc ctgttgctg 1140
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68 gcctgacgcc agagcccagg gaggaccgtg agggggatga cctcaccctg cacagcttcc 1260
70 tcccttagct cactctgcca tctgttttgg caagacccca cctccacggg ctctcctggg 1320
72 ccaacctgta gtgcccagc cccaatccac agctctgggc ttctcggag acccctggag 1380
74 atggggatct tcagggaggg aactctggcc acccaaacg gacaagagca gcctggggcc 1440
76 aagcagacgg tcaagtggag ccacctctt cctcccctcg cggatgaagc ccagcccat 1500
78 ttcagccgag gtccaaggca ggaggccatt tacttgagac agattctctc ctttttctctg 1560
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82 actggagtct cctcccctg tacccaagg 1649
85 <210> SEQ ID NO: 2
86 <211> LENGTH: 402

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88 <213> ORGANISM: Homo sapiens
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94 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
95           20           25           30
97 Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
98           35           40           45
100 Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
101           50           55           60
103 Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
104  65           70           75           80
106 Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
107           85           90           95
109 Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
110           100          105          110
112 Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
113           115          120          125
115 Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr
116           130          135          140
118 Arg Leu Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu
119 145           150          155          160
121 Ala Gln Thr Thr Pro Pro Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro
122           165          170          175
124 Thr Gly Leu Glu Ala Gln Thr Thr Ala Pro Ala Ala Met Glu Ala Gln
125           180          185          190
127 Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Pro Pro Ala Ala
128           195          200          205
130 Met Glu Ala Gln Thr Thr Gln Thr Thr Ala Met Glu Ala Gln Thr Thr
131           210          215          220
133 Ala Pro Glu Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu
134 225           230          235          240
136 Ala Gln Thr Thr Pro Leu Ala Ala Met Glu Ala Leu Ser Thr Glu Pro
137           245          250          255
139 Ser Ala Thr Glu Ala Leu Ser Met Glu Pro Thr Thr Lys Arg Gly Leu
140           260          265          270
142 Phe Ile Pro Phe Ser Val Ser Ser Val Thr His Lys Gly Ile Pro Met
143           275          280          285
145 Ala Ala Ser Asn Leu Ser Val Asn Tyr Pro Val Gly Ala Pro Asp His
146           290          295          300
148 Ile Ser Val Lys Gln Cys Leu Leu Ala Ile Leu Ile Leu Ala Leu Val
149 305           310          315          320
151 Ala Thr Ile Phe Phe Val Cys Thr Val Val Leu Ala Val Arg Leu Ser
152           325          330          335
154 Arg Lys Gly His Met Tyr Pro Val Arg Asn Tyr Ser Pro Thr Glu Met
155           340          345          350
157 Val Cys Ile Ser Ser Leu Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala
158           355          360          365

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160 Thr Ala Asn Gly Gly Leu Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro
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163 Glu Pro Arg Glu Asp Arg Glu Gly Asp Asp Leu Thr Leu His Ser Phe
164 385                      390                      395                      400
166 Leu Pro
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171 <211> LENGTH: 942
172 <212> TYPE: DNA
173 <213> ORGANISM: Homo sapiens
175 <220> FEATURE:
176 <221> NAME/KEY: CDS
177 <222> LOCATION: (1)..(939)
179 <400> SEQUENCE: 3
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181 Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
182 1 5 10 15
184 agc ttg cag ctg tgg gac acc tgg gca gat gaa gcc gag aaa gcc ttg 96
185 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
186 20 25 30
188 ggt ccc ctg ctt gcc cgg gac cgg aga cag gcc acc gaa tat gag tac 144
189 Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
190 35 40 45
192 cta gat tat gat ttc ctg cca gaa acg gag cct cca gaa atg ctg agg 192
193 Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
194 50 55 60
196 aac agc act gac acc act cct ctg act ggg cct gga acc cct gag tct 240
197 Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
198 65 70 75 80
200 acc act gtg gag cct gct gcg cgg ccg cac aca tgc cca ccg tgc cca 288
201 Thr Thr Val Glu Pro Ala Ala Arg Pro His Thr Cys Pro Pro Cys Pro
202 85 90 95
204 gca cct gaa gcc ctg ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa 336
205 Ala Pro Glu Ala Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
206 100 105 110
208 ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg 384
209 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
210 115 120 125
212 gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac 432
213 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
214 130 135 140
216 gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag 480
217 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
218 145 150 155 160
220 cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac 528
221 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
222 165 170 175
224 cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa 576
225 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
226 180 185 190

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228 gcc ctc cca gtc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag 624
229 Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
230      195      200      205
232 ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg 672
233 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
234      210      215      220
236 acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc 720
237 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
238 225      230      235      240
240 agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac 768
241 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
242      245      250      255
244 tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc 816
245 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
246      260      265      270
248 tat agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc 864
249 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
250      275      280      285
252 ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag 912
253 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
254      290      295      300
256 aag agc ctc tcc ctg tcc ccg ggt aaa tga 942
257 Lys Ser Leu Ser Leu Ser Pro Gly Lys
258 305      310
261 <210> SEQ ID NO: 4
262 <211> LENGTH: 313
263 <212> TYPE: PRT
264 <213> ORGANISM: Homo sapiens
266 <400> SEQUENCE: 4
267 Met Pro Leu Gln Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
268 1      5      10      15
270 Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
271      20      25      30
273 Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
274      35      40      45
276 Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
277      50      55      60
279 Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
280 65      70      75      80
282 Thr Thr Val Glu Pro Ala Ala Arg Pro His Thr Cys Pro Pro Cys Pro
283      85      90      95
285 Ala Pro Glu Ala Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys
286      100      105      110
288 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
289      115      120      125
291 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
292      130      135      140
294 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
295 145      150      155      160

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297 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
298           165           170           175
300 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
301           180           185           190
303 Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
304           195           200           205
306 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
307           210           215           220
309 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
310 225           230           235           240
312 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
313           245           250           255
315 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
316           260           265           270
318 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
319           275           280           285
321 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
322           290           295           300
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/825,580

DATE: 04/19/2001

TIME: 12:17:57

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\04192001\I825580.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date